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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN THE PATENT APPLICATION OF

HARBERD et al

Atty. Ref.: 620-157

Serial No.: 09/911,513

Group Art Unit: 1638

Filed: July 25, 2001

Examiner: Mehta, A.

For: NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA

10
Formal
Drawings

* * * * *

December 19, 2002

SUBMISSION OF FORMAL DRAWINGS

Hon. Commissioner of Patents
and Trademarks
Washington, DC 20231

Attn: Official Draftsperson

Sir:

Enclosed herewith are 13 sheets of formal, inked drawings for the above-identified application.

Respectfully submitted,

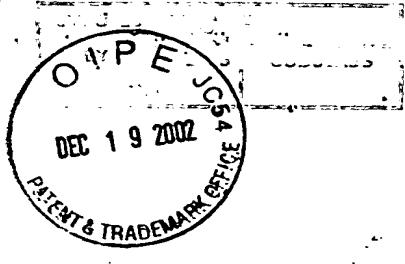
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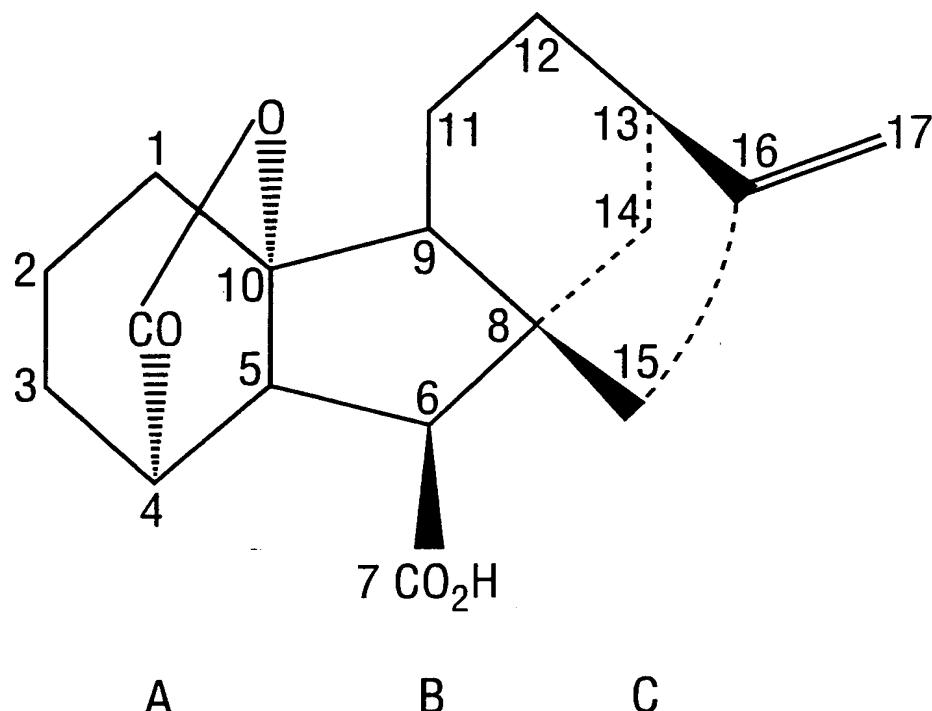
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FIG. 1





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FIG. 2a

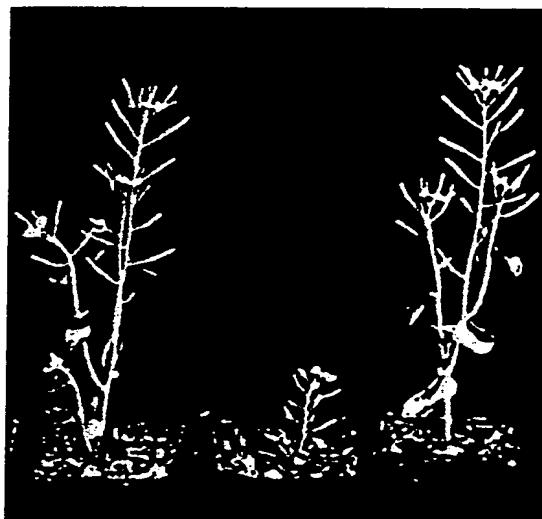


FIG. 2b

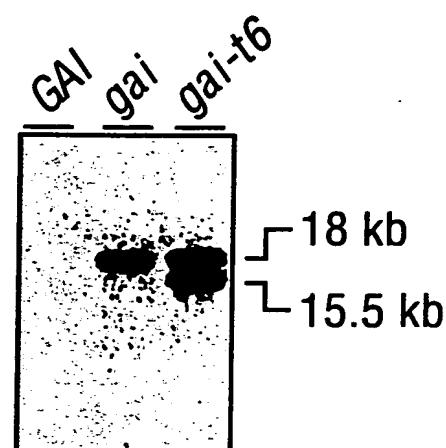
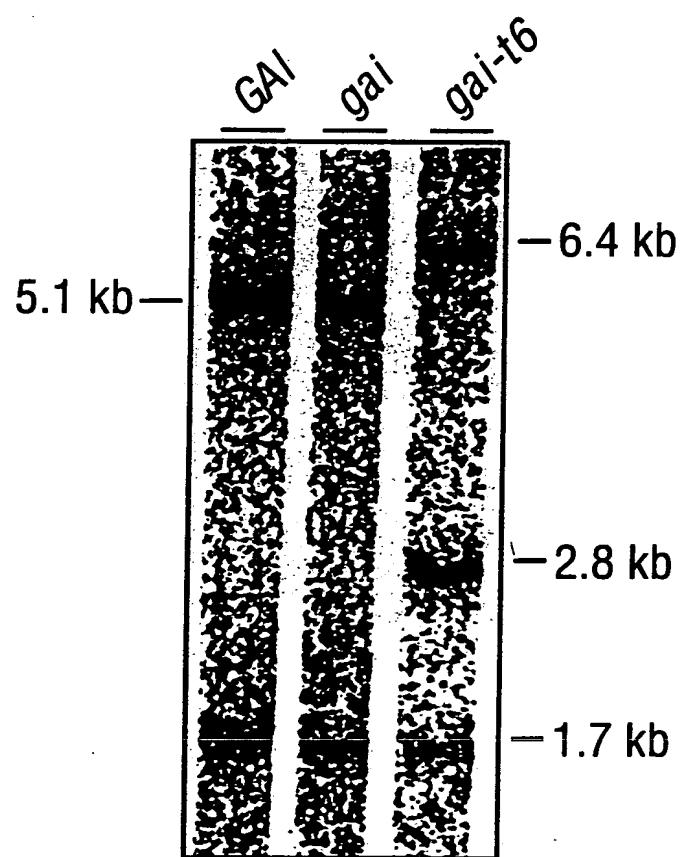


FIG. 2c



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Figure 3

TAATAATCAT TTTTTTCTT ATAACCTTCC TCTCTATT TACAATTAT TTTGTTATTA	60
GAAGTGGTAG TGGAGTGAAA AAACAAATCC TAAGCAGTCC TAACCGATCC CCGAAGCTAA	120
AGATTCTCA CCTTCCAAA TAAAGCAAAA CCTAGATCCG ACATTGAAGG AAAAACCTT	180
TAGATCCATC TCTGAAAAAA AACCAACCAT GAAGAGAGAT CATCATCATC ATCATCAAGA	240
TAAGAAGACT ATGATGATGA ATGAAGAAGA CGACGGTAAC GGCATGGATG AGCTTCTAGC	300
TGTTCTTGGT TACAAGGTTA GGTACATCGGA AATGGCTGAT GTTGCTCAGA AACTCGAGCA	360
GCTTGAAGTT ATGATGTCTA ATGTTCAAGA AGACGATCTT TCTCAACTCG CTACTGAGAC	420
TGTTCACTAT AATCCGGCGG AGCTTACAC GTGGCTTGAT TCTATGCTCA CCGACCTTAA	480
TCCTCCGTCG TCTAACGCCG AGTACGATCT TAAAGCTATT CCCGGTGACG CGATTCTCAA	540
TCAGTTCGCT ATCGATTCCG CTTCTTCGTC TAACCAAGGC GGCGGAGGAG ATACGTATAC	600
TACAAACAAG CGGTTGAAAT GCTCAAACGG CGTCGTGGAA ACCACCACAG CGACGGCTGA	660
GTCAACTCGG CATGTTGTCC TGTTGACTC GCAGGAGAAC GGTGTGCGTC TCGTCACGC	720
GCTTTGGCT TGGCCTGAAG CTGTTCAGAA GGAGAATCTG ACTGTGGCGG AAGCTCTGGT	780
GAAGCAAATC GGATTCTTAG CTGTTCTCA AATCGGAGCT ATGAGAAAAG TCGCTACTTA	840
CTTCGCCGAA GCTCTCGCGC GGCGGATTAA CCGTCTCTCT CCGTCGCAGA GTCCAATCGA	900
CCACTCTCTC TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCCCTT ATCTCAAGTT	960
CGCTCACTTC ACGCGAATC AAGCGATTCT CGAAGCTTT CAAGGGAAGA AAAGAGTTCA	1020
TGTCATTGAT TTCTCTATGA GTCAAGGTCT TCAATGCCG GCGCTTATGC AGGCTCTTGC	1080
GCTTCGACCT GGTGGTCCTC CTGTTTCCG GTTAACCGGA ATTGGTCCAC CGGCACCGGA	1140
TAATTCGAT TATCTTCATG AAGTTGGGTG TAAGCTGGCT CATTAGCTG AGGCGATTCA	1200
CGTTGAGTTT GAGTACAGAG GATTGTGGC TAACACTTTA GCTGATCTT ATGCTTCGAT	1260
GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTT TCGAGCTTCA	1320
CAAGCTCTG GGACGACCTG GTGCGATCGA TAAGGTTCTT GGTGTGGTGA ATCAGATTAA	1380
ACCGGAGATT TTCACTGTGG TTGACCGAGA ATCGAACCAT AATAGTCCGA TTTCTTAGA	1440
TCGGTTTACT GAGTCGTTGC ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC	1500
GAGTGGTCAA GACAAGGTCA TGTCGGAGGT TTACTGGGT AAACAGATCT GCAACGTTGT	1560
GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT GGAGGAACCG	1620
GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCG AATGCGTTTA AGCAAGCGAG	1680
TATGCTTTG GCTCTGTTCA ACGGCCGTGA GGGTTATCGG GTGGAGGAGA GTGACGGCTG	1740
TCTCATGTTG GGTGGCACA CACGACCGCT CATAGCCACC TCGGCTTGGA AACTCTCCAC	1800
CAATTAGATG GTGGCTCAAT GAATTGATCT GTTGAACCGG TTATGATGAT AGATTCCGA	1860
CCGAAGCCAA ACTAAATCCT ACTGTTTTTC CCTTTGTCAC TTGTTAAGAT CTTATCTTTC	1920
ATTATATTAG GTAATTGAAA AATTCTAAA TTACTCACAC TGGC	1964

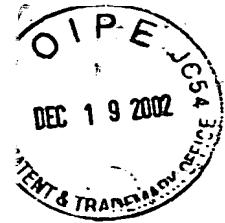


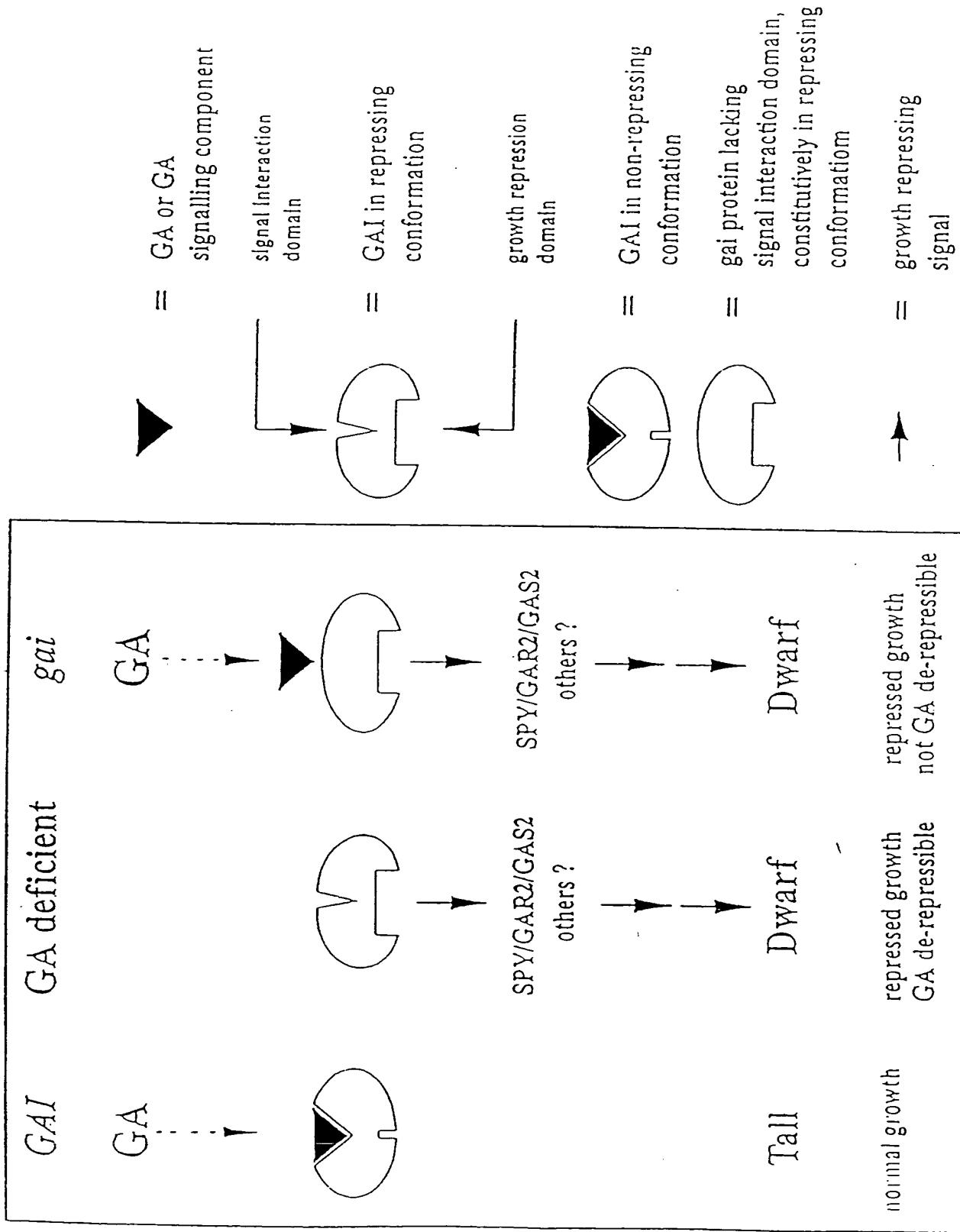
Figure 4

MetLysArgAspHisHisHisHisGlnAspLysLysThrMetMetMetAsnGluGlu	20
AspAspGlyAsnGlyMetAspGluLeuLeuAlaValLeuGlyTyrLysValArgSerSer	40
<u>Glu</u> MetAlaAspValAlaGlnLysLeuGluGlnLeuGluValMetMetSerAsnValGln	60
GluAspAspLeuSerGlnLeuAlaThrGluThrValHisTyrAsnProAlaGluLeuTyr	80
ThrTrpLeuAspSerMetLeuThrAspLeuAsnProProSerSerAsnAlaGluTyrAsp	100
LeuLysAlaIleProGlyAspAlaIleLeuAsnGlnPheAlaIleAspSerAlaSerSer	120
SerAsnGlnGlyGlyGlyAspThrTyrThrAsnLysArgLeuLysCysSerAsn	140
GlyValValGluThrThrAlaThrAlaGluSerThrArgHisValValLeuValAsp	160
SerGlnGluAsnGlyValArgLeuValHisAlaLeuLeuAlaCysAlaGluAlaValGln	180
LysGluAsnLeuThrValAlaGluAlaLeuValLysGlnIleGlyPheLeuAlaValSer	200
GlnIleGlyAlaMetArgLysValAlaThrTyrPheAlaGluAlaLeuAlaArgArgIle	220
TyrArgLeuSerProSerGlnSerProIleAspHisSerLeuSerAspThrLeuGlnMet	240
HisPheTyrGluThrCysProTyrLeuLysPheAlaHisPheThrAlaAsnGlnAlaIle	260
LeuGluAlaPheGlnGlyLysLysArgValHisValIleAspPheSerMetSerGlnGly	280
LeuGlnTrpProAlaLeuMetGlnAlaLeuAlaLeuArgProGlyGlyProProValPhe	300
ArgLeuThrGlyIleGlyProProAlaProAspAsnPheAspTyrLeuHisGluValGly	320
CysLysLeuAlaHisLeuAlaGluAlaIleHisValGluPheGluTyrArgGlyPheVal	340
AlaAsnThrLeuAlaAspLeuAspAlaSerMetLeuGluLeuArgProSerGluIleGlu	360
SerValAlaValAsnSerValPheGluLeuHisLysLeuLeuGlyArgProGlyAlaIle	380
AspLysValLeuGlyValValAsnGlnIleLysProGluIlePheThrValValGluGln	400
GluSerAsnHisAsnSerProIlePheLeuAspArgPheThrGluSerLeuHisTyrTyr	420
SerThrLeuPheAspSerLeuGluGlyValProSerGlyGlnAspLysValMetSerGlu	440
ValTyrLeuGlyLysGlnIleCysAsnValValAlaCysAspGlyProAspArgValGlu	460
ArgHisGluThrLeuSerGlnTrpArgAsnArgPheGlySerAlaGlyPheAlaAlaAla	480
HisIleGlySerAsnAlaPheLysGlnAlaSerMetLeuLeuAlaLeuPheAsnGlyGly	500
GluGlyTyrArgValGluGluSerAspGlyCysLeuMetLeuGlyTrpHisThrArgPro	520
LeuIleAlaThrSerAlaTrpLysLeuSerThrAsn	532



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Figure 5





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Figure 6(a)

1 TAGAAGTGGT AGTCGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAAACTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCC GG TGAC GCGATTCTCA ATCAGTTCGC TATCGATTG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATAAGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCAACCACA GCGACGGCTG
551 AGTCAAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
601 CTCGTTCACG CGCTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGC GG ATT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTITAGATGC ACTTCTACGA GACTTGTCCCT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAAG
901 AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTCATGGCC
951 GGCGCTTATG CAGGCTCTTG CGCTTCGACC TGGTGGTCCT CCTGTTTCC
1001 GGTAAACCGG AATTGGTCCA CCGGCACCGG ATAATTTCGA TTATCTTCAT
1051 GAAGTTGGGT GTAAGCTGGC TCATTTAGCT GAGGCGATTC ACgtTGAGTT
1101 TGAGTACAGA GGATTGTGG CTAACACTTT AGCTGATCTT GATGCTTCGA
1151 TGCTTGAGCT TAGACCAAGT GAGATTGAAT CTGTTGCGGT TAACTCTGTT
1201 TTGAGCTTC ACAAGCTCTT GGGACGACCT GGTGCGATCG ATAAGGTTCT
1251 TGGTGTGGTG AATCAGATTA AACCGGAGAT TTTCACTGTG GTTGAGCAGG
1301 AATCGAACCA TAATAGTCCG ATTTCTTAG ATCGGTTTAC TGAGTCGTTG
1351 CATTATTACT CGACGTTGTT TGACTCGTTG GAAGGTGTAC CGAGTGGTCA
1401 AGACAAGGTC ATGTCGGAGG TTTACTTGGG TAAACAGATC TGCAACGTTG
1451 TGGCTTGTGA TGGACCTGAC CGAGTTGAGC GTCATGAAAC GTTGAGTCAG
1501 TGGAGGAACC GTTCTGGGTC TGCTGGTTT CGGGCTGCAC ATATTGGTTC
1551 GAATGCCCTT AAGCAAGCGA GTATGCTTTT GGCTCTGTTC AACGGCGGTG
1601 AGGGTTATCG GCTGGAGGAG AGTGAACGGCT GTCTCATGTT CCC



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Figure 6(b)

1 MKRDHHHHHQ DKKTMMNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSDL TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTINKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT L*



Figure 6(c)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCC GG TGAC GCGATTCTCA ATCAGTTCGC TATCGATTG
451 GCTTCTTCGT CTAACCAAGG CGGC GGAGGA GATA CGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGT CGTGGA AACCA ACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGT GTGCGT
601 CTCGTTCACCG CGCTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGGGGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTT CAGATGC ACTTCTACGA GACTTGTCTT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTG TCGAAGCTTT TCAAGGGAAAG
901 AAAAGAGTTC ATGTCATTGA TTCTCTATGA GTCAAGGTCT TCAATGGCCG
951 GCGCTTATGC AGGCTTTGC GCTTCGACCT GGTGGTCCTC CTGTTTCCG
1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTCGAT TATCTTCATG
1051 AAGTTGGGTG TAAGCTGGCT CATTAGCTG AGGCGATTCA CGTTGAGTTT
1101 GAGTACAGAG GATTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTTT
1201 TCGAGCTTCA CAAGCTTTG GGACGACCTG GTGCGATCGA TAAGGTTCTT
1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
1301 ATCGAACCAT AATAGTCCGA TTTCTTAGA TCGGTTTACT GAGTCGTTGC
1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GACTGGTCAA
1401 GACAAGGTCA TGTGGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT
1451 GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATCAAACG TTGAGTCAGT
1501 GGAGGAACCG GTTGGGGTCT GCTGGTTTG CGGCTGCACA TATTGGTTCG
1551 AATGCGTTA AGCAAGCGAG TATGCTTTG GCTCTGTTCA ACGGCGGTGA
1601 GGGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG



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Figure 6(d)

1 MKRDHHHHHQ DKKTMMNNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILEAFQGK
251 KRVHVIDSL*



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Figure 6(e)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCC GG TGAC GCGATTCTCA ATCAGTTCGC TATCGATTCG
451 GCTTCTTCGT CTAACCAAGG CGGGGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
601 CTCGTTCACG CGCTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGCGGATT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTTCAAGATGC ACTTCTACGA GACTTGTCCCT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
901 AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTGGGCGCTT
951 ATGCAGGCTC TTGCGCTTCG ACCTGGTGGT CCTCCTGTTT TCCGGTTAAC
1001 CGGAATTGGT CCACCGGCAC CGGATAATT CGATTATCTT CATGAAGTTG
1051 GGTGTAAGCT GGCTCATTAA GCTGAGGCGA TTCACGTTGA GTTGAGTAC
1101 AGAGGATTG TGGCTAACAC TTTAGCTGAT CTTGATGCTT CGATGCTTGA
1151 GCTTAGACCA AGTGAGATTG AATCTGTTGC GGTAACTCT GTTTTCGAGC
1201 TTCACAAGCT CTTGGGACGA CCTGGTGCAG TCGATAAGGT TCTTGGTGTG
1251 GTGAATCAGA TTAAACCGGA GATTTCACT GTGGTTGAGC AGGAATCGAA
1301 CCATAATAGT CCGATTCTCT TAGATCGGTT TACTGAGTCG TTGCATTATT
1351 ACTCGACGTT GTTGACTCG TTGGAAGGTG TACCGAGTGG TCAAGACAAG
1401 GTCATGTCGG AGGTTACTT GGGTAAACAG ATCTGCAACG TTGTGGCTTG
1451 TGATGGACCT GACCGAGTTG AGCGTCATGA AACGTTGAGT CAGTGGAGGA
1501 ACCGGTTCGG GTCTGCTGGG TTTGCGGCTG CACATATTGG TTCGAATGCG
1551 TTTAAGCAAG CGAGTATGCT TTTGGCTCTG TTCAACGGCG GTGAGGGTTA
1601 TCGGGTGGAG GACAGTGACG GCTGTCTCAT GTTGGG



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Figure 6(f)

1 MKRDHHHHHQ DKKTMMMNNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILEAFQGK
251 KRVHVIDFSM SQGLGRLCRL LRFDLVVLLF SG*



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Figure 6(g)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAACAGT CCTAACCGAT
51 CCCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCAGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCAACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTGTCC TGGTTGACTC GCAGGAGAAC GGTGTGCGTC
601 TCGTTCACGC GCTTTGGCT TGCGCTGAAG CTGTTCAGAA GGAGAATCTG
651 ACTGTGGCGG AAGCTCTGGT GAAGCAAATC GGATTCTTAG CTGTTCTCA
701 AATCGGAGCT ATGAGAAAAG TCGCTACTTA CTTCGCCGAA GCTCTCGCGC
751 GGCAGGATTAA CCGTCTCTCT CCGTCGCAGA GTCCAATCGA CCACCTCTC
801 TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCCCT ATCTCAAGTT
851 CGCTCACTTC ACGGCGAATC AAGCGATTCT CGAAGCTTT CAAGGGAAAGA
901 AAAGAGTTCA TGTCAATTGAT TTCTCTATGA GTCAAGGTCT TCAATGGCCG
951 GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCTC CTGTTTCCG
1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTCGAT TATCTTCATG
1051 AAGTTGGGTG TAAGCTGGCT CATTAGCTG AGGCGATTCA CGTTGAGTTT
1101 GAGTACAGAG GATTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTTT
1201 TCGAGCTTCA CAAGCTCTTG CGACGACCTG GTCGATCGA TAAGGTTCTT
1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
1301 ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
1401 GACAAGGTCA TGTCGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT
1451 GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
1501 GGAGGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCG
1551 AATGCGTTA AGCAAGCGAG TATGCTTTG GCTCTGTTCA ACGGCAGGTGA
1601 GGGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG



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Figure 6(h)

1 MKRDHHHHHQ DKKTMMNNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTINKRLK CSNGVVEETT ATAESTRHVS WLTRRRRTVCV
151 SFTRFWLALK LFRRRI*